WHAT IS CLAIMED IS:

1. A method of quantitating the amount of a protein or peptide in a sample comprising:

   (a) obtaining a sample containing said protein or peptide;

   (b) providing a standard protein or peptide wherein the standard is a derivative of the protein or peptide of interest at a known or measurable quantity;

   (c) co-crystallizing the protein or peptide and standard with a matrix;

   (d) analyzing the crystallized target protein or peptide and standard using matrix-assisted laser dissorption/ionization time of flight (MALDI-TOF) mass spectrometry; and

   (e) determining the amount of the protein or peptide present in the sample based on the analysis in (d).

2. The method of claim 1, wherein said sample is derived from a cell.

3. The method of claim 2, wherein said cell is a prokaryotic cell.

4. The method of claim 2, wherein said cell is a eukaryotic cell.

5. The method of claim 2, wherein said cell is a mammalian cell.

6. The method of claim 2, wherein said cell is a human cell.

7. The method of claim 6, wherein said human cell is a cardiomyocte.

8. The method of claim 1, wherein said sample is derived from an organ.

9. The method of claim 8, wherein said organ is a heart.

10. The method of claim 8, wherein said sample is organ is a human heart.

11. The method of claim 1, wherein said sample is obtained from plasma.

12. The method of claim 1, wherein said sample is obtained from serum.

13. The method of claim 1, wherein said source has been exposed to an agent that alters the expression or structure of the protein or peptide.

14. The method of claim 1, wherein the protein is alpha myosin heavy chain.

15. The method of claim 1, wherein the protein is beta myosin heavy chain.

16. The method of claim 1, wherein the protein is cardiac actin.

17. The method of claim 1, wherein the protein is skeletal actin.

18. The method of claim 1, wherein the peptide is produced by proteolytic cleavage.

19. The method of claim 1, wherein the peptide is produced by chemical cleavage.

20. The method of claim 1, wherein the peptide is produced by enzymatic digestion.

21. The method of claim 20, wherein the enzymatic digestion is performed by an endopeptidase.

22. The method of claim 20, wherein the enzymatic digestion is performed by a protease.

23. The method of claim 1, wherein the protein, peptide and/or standard are produced synthetically.

24. The method of claim 1, wherein the standard is designed by modifying a single amino acid from the target protein or peptide.

25. A method of quantitatively comparing the amount of a plurality of structurally distinct proteins or peptides in a sample comprising:

(a) obtaining one or more samples containing said multiply distinct target proteins or peptides;

(b) providing a standard protein or peptide for each target protein, wherein the standard is a derivative of the target protein or peptide of interest at a known or measurable quantity;

(c) co-crystallizing the target proteins or peptides and standard with a matrix;

(d) analyzing the crystallized target proteins or peptides and standard using matrix-assisted laser dissorption/ionization time of flight (MALDI-TOF) mass spectrometry; and

(e) determining relative or absolute amounts of each target protein or peptide analyzed that is present in the sample.

26. The method of claim 25, wherein the proteins are isoforms of each other.

27. The method of claim 26, wherein the isomers are phosphoisomers.

28. The method of claim 25, wherein said sample is derived from a cell.

29. The method of claim 28, wherein said cell is a prokaryotic cell.

30. The method of claim 28, wherein said cell is a eukaryotic cell.

31. The method of claim 28, wherein said cell is a mammalian cell.

32. The method of claim 28, wherein said cell is a human cell.

33. The method of claim 32, wherein said human cell is a cardiomyocte.

34. The method of claim 25, wherein said sample is derived from an organ.

35. The method of claim 34, wherein said sample organ is a heart.

36. The method of claim 34, wherein said organ is a human heart.

37. The method of claim 25, wherein said sample is obtained from plasma.

38. The method of claim 25, wherein said sample is obtained from serum.

39. The method of claim 25, wherein said source has been exposed to an agent that alters the expression or structure of the proteins or peptides.

40. The method of claim 25, wherein one of the proteins is α-myosin heavy chain.

41. The method of claim 25, wherein one of the proteins is β-myosin heavy chain.

42. The method of claim 25, wherein one of the proteins is cardiac actin.

43. The method of claim 25, wherein one of the proteins is skeletal actin.

44. The method of claim 25, wherein the peptides are produced by proteolytic cleavage.

45. The method of claim 25, wherein the peptides are produced by chemical cleavage.

46. The method of claim 25, wherein the peptides are produced by enzymatic digestion.

47. The method of claim 46, wherein the enzymatic digestion is performed by an endopeptidase.

48. The method of claim 46, wherein the enzymatic digestion is performed by a protease.

49. The method of claim 25, wherein the proteins, peptides and/or standards are produced synthetically.

50. The method of claim 25, wherein the standards are proteins or peptides derived or synthesized directly from the proteins of interest.

51. The method of claim 25, wherein the standard are designed by modifying a single amino acid from the target proteins or peptides.

52. A method of determining relative amounts of at least two distinct proteins or peptides in a sample comprising:

(a) obtaining a samples containing said multiply distinct target proteins or peptides;
(b) co-crystallizing the target proteins or peptides and standard with a matrix;
(c) analyzing the crystallized target proteins or peptides using matrix- assisted laser dissorption/ionization time of flight (MALDI-TOF) mass spectrometry; and
(d) determining the relative amount of each target protein or peptide analyzed that is present in the sample.